

FIG. 1A

1	CGCCAAACCTCTATGGATATATAAGGGAAGCTTGAGGAGGAATTTCACAGTTACAGTGC	60
61	AGAAGCAGAGGCAAAAGAAATTAAACAGCTCTTCAGTCAAGCAAAATCCTCTACTCACCATG	120
	<u>M</u>	1
121	CTTCCTCCTGCCATTTCATTCTATCTCCTTCCCTTGCAATGCAATGAAAAAGCTGT	180
2	<u>L P P A I H F Y L L P L A C I L M K S C</u>	21
181	TTGGCTTTTAAAAATGATGCCACAGAAAATCCTTTATTCACATGTGGTTAAACCTGTTCCA	240
22	<u>L A F K N D A T E I L Y S H V V K P V P</u>	41
241	GCACACCCAGCAGCAACAGCACGTTGAATCAAGCCAGAAATGGAGGCAGGCATTTCAGT	300
42	A H P S S N S T L N Q A R N G G R H F S	61
301	AACACTGGACTGGATCGGAACACTCGGGTTCAAGTGGGTTGCCGGGAACTGCCGTTCCACC	360
62	N T G L D R N T R V Q V G C R E L R S T	81
361	AAATACATCTCTGATGGCCAGTGCCAGCATCAGCCCTCTGAAGGAGCTGGTGTGTGCT	420
82	K Y I S D G Q C T S I S P L K E L V C A	101

FIG. 1B

421 GCGAGTGTCTTGTCCCTGCGAGTGTCCCTAACTGGATTGGAGGAGGCTATGGAACAAAG 480
 102 G E C L P L P V L P N W I G G G Y G T K 121

 481 TACTGGAGCAGGAGGAGCTCCCAGGAGTGGCGGTGTGTCAATGACAAAACCCGTACCCAG 540
 122 Y W S R R S S Q E W R C V N D K T R T Q 141

 541 AGAATCCAGCTGCAGTGCCCAAGATGGCAGCACACGCACCTACAAAATCACAGTAGTCACT 600
 142 R I Q L Q C Q D G S T R T Y K I T V V T 161

 601 GCCTGCAAGTGCAAGAGGTACACCCGGCAGCACAAACGAGTCCAGTCACAACTTTTGAGAGC 660
 162 A C K C K R Y T R Q H N E S S H N F E S 181

 661 ATGTCACCTGCCCAAGCCAGTCCAGCATCACAGAGAGCGGAAAAGAGCCAGCAAAATCCAGC 720
 182 M S P A K P V Q H H R E R K R A S K S S 201

 721 AAGCACAGCATGAGTTAGAACTCAGACTCCCCATAACTAGACTTACTAGTAACCATCTGCT 780
 202 K H S M S * 206

 781 TTACAGATTGTGCTTGGAAGACTCAAGCCTGCCACTGCTGTGTTTCTCACTTGAAAGT 840
 841 ATATGCTTTCCTGCTTTGATCAAAACCCAGCAAGCTGTCTTAAAGTATCAGGACCTTCTTTGG 900

FIG. 2A

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1..... 50
  ..... M SSSTFRTLAV AVTLLHLTRL AL.STCP... ..AACHCP..
  ..... M SSRIVRELAL VVTLLHLTRV GL.STCP... ..ADCHCP..
  ..... M GSAGARP.AL AAALLCLARL ALGSPCP... ..AVCQCP..
  ..... MTA ASMGVVRVAF VVLLALCSRP AVQNC... ..GPCRCPD.
  ..... MLA SVAGPISLAL .VLLALCTRP ATGQDCS... ..AQCQCAA.
  METGG... ..QGLPVLL LLLLLLRPCE VSGREAA... ..CPRPCGGR
  MQSVQSTSFC LRKQCLCLTF LLLHLLGQVA ATQR... ..CPQCPGR
  ..... MKSVL LLTTLLVPAH LVAAWSNNYA VDCPQHCDSS
  ..... MQR ARPTLWAAAL TLLVLLRGPP VARAGASSG LGPVVRCEPC
  .....
  SCGF .....

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111..... 160
  ..... TALKGICRAQ SEGRPCEYNS RIYQNGESFQ PNCKHQCTCI
  ..... TALKGICRAQ SEGRPCEYNS RIYQNGESFQ PNCKHQCTCI
  ..... AATNGICRAQ SEGRPCEYNS KIYQNGESFQ PNCKHQCTCI
  GLFCDFGSPA NRKIGVCTAK .DGAPCIFGG TVYRSGESFQ SSCKYQCTCL
  GLFCDFGSPA NRKIGVCTAK .DGAPCVFVG SVYRSGESFQ SSCKYQCTCL
  GLYCDRGPED GGGAGICMVL .EGDNCVFDG MIYRNGETFQ PSCKYQCTCR
  GLYCDRSADP SNQTGICTAV .EGDNCVFDG VIYRSGEKFQ PSCKFQCTCR
  GE...DPFG EEFGICKDCP YGT...FG MDCRETCNCQ SGICDRGTGK
  DEARPLQALL DGRGLCVNAS AVSRLRAYLL PAPPAPGNAS ESEEDRSAGS
  .....
  SCGF .....

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FIG. 2B

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51.....110
..LEAPKCAP GVGLVR.... DGCGCKVC AKQLNED.... C SKTQPCDHTK
..LEAPKCAP GVGLVR.... DGCGCKVC AKQLNED.... C RKTQPCDHTK
..AAPQCAP GVGLVP.... DGCGCKVC AKQLNED.... C SRTQPCDHTK
..EPAPRCPA GVSLVL.... DGCGCCRV AKQLGEL.... C TERDPCDPHK
..EAPHCPA GVSLVL.... DGCGCCRV AKQLGEL.... C TERDPCDPHK
CPAEPKCAP GVPAVL.... DGCGCCCLVC ARQGES.... C SPLPCDESG
CPATPPTCAP GVR AVL.... DGSCCCLVC ARQGES.... C SDLEPCDESS
ECKSSPRCKR TVL..... DDCGCCRV AAGRGETCYR TVSGMDGMKC GGLRCQPSN
DARALAQCAP PPAVCAELVR EPGCGCCLTC ALSEGQPC.. GIYTERC GGLRCQPSP
.....

161.....220
D.GAVGCIPL CPQELSLPNL GCPNPRLVKV SGQCCCEWVC DEDSIKDSLD DQDDL....L
GWRGACIPL CPQELSLPNL GCPNPRLVKV TGQCCCEWVC DEDSIKDPME DQDGLLGKGL
D.GAVGCIPL CPQELSLPNL GCPSPRLVKV PGQCCCEWVC DES..KDALE ELEGFFSKEF
D.GAVGCMPL CSMDVRLPSP DCPFPRRVKL PGKCCCEWVC DEP..... KDQTVVGP
D.GAVGCVPL CSMDVRLPSP DCPFPRRVKL PGKCCKEWVC DEP..... KDR TAVGP
D.GQIGCLPR CNLGLLLPGP DCPFPRKIEV PGECCEKWVC DPR..... DEVLLGGF
D.GQIGCVPR CQLDVLLPEP NCPAPRKVEV PGECCEKWIC GPD..... FEEDSLGGL
CL..... KFPFFQYS VTKSSNRFVS LTHEDMASGD GNIVREEVVK
VESPSVSSSTH RVSDPKFHPL HSKIIIIKKG HAKDSQRYK.. VDYESQSTD TQNFSSSKR
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FIG 2.C

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221..... 270
cyr6_mouse GLDASEVELT RNNELIAIGK GSSLKRLLPVF GTEP.:RVLF NPLHAHQKC
      HCGF GFDASEVELT RNNELIAVGK GSSLKRLLPVF GMEP..RILY NPL...QGQKC
ce10_chick GLDASEGELT RNNELIAIVK G.GLKMLPVF GSEPQSAFE NP.....KC
ctgf_human ALAAAYRLEDT .....F GPDPTMI... ..RANC
fisp-12 ALAAAYRLEDT .....F GPDPTMM... ..RANC
nov_chick AMAAYRQEAT .....L GIDVSDS... ..SANC
      HNGF TLAAAYRPEAT .....L GVEVSDS... ..SVNC
      VIGF ENAAGSPVMR KWLNPR..... ..
ibp3_human ETEYGPCRRE MEDTLNHLKF LNVLSPRGVH IPNCDKKGFY KKKQCRPSKG
      SCGF ...MLPPATH FYLLPLACIL MKSCLAFKND ATEILYSHVV KVPAPHPSSN

331..... 380
cyr6_mouse TKKSPEPVRF TYAGCSSVKK YRPKYCGSCV DGRCCCTPLQT RTVKMRFRCE
      HCGF TKKSPEPVRF TYAGCLSVKK YRPKYCGSCV DGRCCCTPQLT RTVKMRFPCE
ce10_chick TKKSPSPVRF TYAGCSSVKK YRPKYCGSCV DGRCCCTPQQT RTVKIRFRCD
ctgf_human TPKISKPIKF ELSGCTSMKT YRAKFCGVCT DGRCCCTPHRT TTLPVEFKCP
fisp-12 TPKIAKPVKF ELSGCTSVKT YRAKFCGVCT DGRCCCTPHRT TTLPVEFKCP
nov_chick TKKSMKAVERF EYKNCTSVQT YKPRYCGLCN DGRCCCTPHNT KTIQVEFRCP
      HNGF TKKSLKAIHL QFKNCTSLHT YKPRFCGVCS DGRCCCTPHNT KTIQAEFQCS
      VIGF ..... ..
ibp3_human ..... ..
      SCGF ...PLPVLP NWIGGGYGTK YWSR...RSS QEWRCVNDKT RTQRIQLQCQ

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FIG 2D

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271..... 330
IVQTTWSQC SKSCGTGIST RVTNDNPECR LVKETRICEV RPCGQPVY.S SLKKGKKCSK
IVQTTWSQC SKTCGTGIST RVTNDNPECR LVKETRICEV RPCGQPVY.S SLKKGKKCSK
IVQTTWSQC SKTCGTGIST RVTNDNPDCK LIKETRICEV RPCGQPSY.A SLKKGKKCTK
LVQTTWSAC SKTCGMGIST RVTNDNASCR LEKQSRLCMV RPCEADLEE. NIKKGKKCIR
LVQTTWSAC SKTCGMGIST RVTNDNTFCR LEKQSRLCMV RPCEADLEE. NIKKGKKCIR
IEQTTWSAC SKSCGMGFST RVTNRNQCE MVKQTRLMM RPCEN..EEP SDKKGKKCIQ
IEQTTWTAC SKSCGMGFST RVTNRNRQCE MLKQTRLMMV RPCEQEPEQP TDKKGKKCLR
.....
RKRGFWCVD KYGQPLPGYT TKGKEDVHCY SMQSK.....
STLNQARNGG RHFSNTGL.D RNTRVQVGCR ELRSTKYISD GQCTISISPLK ELVCAGECL.

381..... 440
DGEFMSKNVM MIQSKKCNYN CPHPNEASFR LYSLFNDIHK FRD.....
DGETFSKNVM MIQSSKCNYN CPHANEAFFP FYRLF.....
DGETFTKSVM MIQSCRCNYN CPHANEA.YP FYRLVNDIHK FRD.....
DGEVMKKNNM FIKTCACHYN CPGDND.IFE SLYYRKMYGD MA.....
DGEIMKKNNM FIKTCACHYN CPGDND.IFE SLYYRKMYGD MA.....
QGKFLKKPMM LINTCVCHGN CPQSNNAFFQ PLDPMSSEAK I.....
PGQIVKKPVM VIGTCTHTN CPKNNEAFLQ ELELKTTRGK M.....
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DGSTRYKIT VVTACKCKRY TRQHNESHN FESMSPAKPV QHHRERKRAS KSSKHSMS

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